encodes a transcription factor of the Myb family. As indicated in Table 2, page 25, of the specification, SEQ ID NO: 2076 encodes the DNA-binding domains provided in SEQ ID NO: 2346 and 2347.

The specification has been amended to remove references to hyperlinks. Claim 1 has been cancelled from the application and rewritten as newly added claims 31-34. Claims 3, 4 and 7 have been cancelled from the application as being drawn to non-elected subject matter. Claims 2 has been amended to remove reference to cancelled claim 1. Claim 5 has been amended to replace reference to cancelled claims 3 and 4 with reference to SEQ ID NO: 2346 and 2347, the DNA-binding domains encoded by the elected DNA sequence. Claims 6 and 13 have been amended to replace reference to cancelled 1 with reference to newly added claims 31-34. Claim 8 has been amended to replace reference to cancelled claims 3 and 4 with reference to claims 5 and 31-34.

It is submitted that support for all the above amendments may be found throughout the specification as originally filed and that none of the amendments constitute new matter. Applicants further submit that the above amendments were not made for reasons of patentability and therefore do not create prosecution history estoppel.

Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The attached page is captioned "**Version with markings to show changes made.**"

Early consideration of the subject application is respectfully requested.

Respectfully submitted,

Janet Sleath

Janet Sleath
Registration No. 37,007

Date: August 1, 2002

SPECKMAN LAW GROUP

Application No. 09/640,211

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

The paragraph beginning on page 17, line 14, has been replaced with the following new paragraph:

--The polynucleotides identified as SEQ ID NOS: 1-591, 1183-1912 and 1931-2106 may contain open reading frames ("ORFs") or partial open reading frames encoding polypeptides. Open reading frames may be identified using techniques that are well known in the art. These techniques include, for example, analysis for the location of known start and stop codons, most likely reading frame identification based on codon frequencies, etc. Suitable tools and software for ORF analysis are available, for example, on the Internet [at http://www.ncbi.nlm.nih.gov/gorf/gorf.html]. Additionally, tools and software for ORF analysis, for example, including GeneWise, available from The Sanger Center, Wellcome Trust Genome Campus, Hinxton, Cambridge, CB10 1SA, United Kingdom; Diogenes, available from Computational Biology Centers, University of Minnesota, Academic Health Center, UMHG Box 43 Minneapolis MN 55455; and GRAIL, available from the Informatics Group, Oak Ridge National Laboratories, Oak Ridge, Tennessee TN, are suitable. Open reading frames and portions of open reading frames may be identified in the polynucleotides of the present invention. Once a partial open reading frame is identified, the polynucleotide may be extended in the area of the partial open reading frame using techniques that are well known in the art until the polynucleotide for the full open reading frame is identified. Thus, open reading frames encoding polypeptides may be identified using the polynucleotides of the present invention.--

The paragraph beginning on page 18, line 30, has been replaced with the following new paragraph:

--Polynucleotide and polypeptide sequences may be aligned, and percentage of identical residues in a specified region may be determined against another polynucleotide or polypeptide sequence, using computer algorithms that are publicly available. Two

exemplary algorithms for aligning and identifying the similarity of polynucleotide sequences are the BLASTN and FASTA algorithms. Polynucleotides may also be analyzed using the BLASTX algorithm, which compares the six-frame conceptual translation products of a nucleotide query sequence (both strands) against a protein sequence database. The similarity of polypeptide sequences may be examined using the BLASTP algorithm. The BLASTN, BLASTX and BLASTP programs are available on the NCBI anonymous FTP server [(ftp://ncbi.nlm.nih.gov) under /blast/executables], and from the National Center for Biotechnology Information (NCBI) National Library of Medicine, Building 38A, Room 8N805, Bethesda, MD 20894, USA. The BLASTN algorithm Version 2.0.4 [Feb-24-1998] and Version 2.0.6 [Sept-16-1998], set to the default parameters described in the documentation and distributed with the algorithm, are preferred for use in the determination of polynucleotide variants according to the present invention. The BLASTP algorithm, is preferred for use in the determination of polypeptide variants according to the present invention. The use of the BLAST family of algorithms, including BLASTN, BLASTP, and BLASTX, is described at NCBI's Internet website [at the URL http://www.ncbi.nlm.nih.gov/BLAST/newblast.html] and in the publication of Altschul et al., *Nucleic Acids Res.* 25:3389-3402, 1997.--

The paragraph beginning on page 19, line 19, has been replaced with the following new paragraph:

--The computer algorithm FASTA is available on the Internet [at the ftp site ftp://ftp.virginia.edu/pub/fasta/], and from the University of Virginia by contacting David Hudson, Assistance Provost for Research, University of Virginia, PO Box 9025, Charlottesville, VA. Version 2.0u4 [February 1996], set to the default parameters described in the documentation and distributed with the algorithm, may be used in the determination of variants according to the present invention. The use of the FASTA algorithm is described in Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444-2448, 1988; and Pearson, *Methods in Enzymol.* 183:63-98, 1990.--

The paragraph beginning on page 23, line 25, has been replaced with the following new paragraph:

--In certain embodiments, the DNA constructs of the present invention include an open reading frame coding for at least a functional portion of a polypeptide of the present invention or a variant thereof. As used herein, the "functional portion" of a polypeptide is that portion which contains the active site essential for regulating gene expression, *i.e.*, the portion of the molecule that is capable of binding to, or interacting with, the promoter of the gene to be expressed. The DNA-binding domain(s) for certain of the inventive polypeptides are identified below in Table 2. These DNA binding domains were identified using PROSITE 15.0 pattern or profile sequences as listed in the PROSITE database. PROSITE is available [at http://www.expasy.ch/sprot/prosite.html] on the Internet and its use is described in Hofman et al., *Nucleic Acids Res.* 27:215-219, 1999; and in Bairoch, *Nucleic Acids Res.* 20:Suppl.2013-2018, 1992.--

The paragraph beginning on page 32, line 22, has been replaced with the following new paragraph:

--In specific embodiments, the oligonucleotide probes and/or primers comprise at least about 6 contiguous residues, more preferably at least about 10 contiguous residues, and most preferably at least about 20 contiguous residues complementary to a polynucleotide sequence of the present invention. Probes and primers of the present invention may be from about 8 to 100 base pairs in length or, preferably from about 10 to 50 base pairs in length or, more preferably from about 15 to 40 base pairs in length. The probes can be easily selected using procedures well known in the art, taking into account DNA-DNA hybridization stringencies, annealing and melting temperatures, and potential for formation of loops and other factors, which are well known in the art. Tools and software suitable for designing probes, and especially suitable for designing PCR primers, are available on the Internet[, for example, at URL http://www.horizonpress.com/pcr/]. A software program suitable for designing probes, and especially for designing PCR primers, is available from Premier Biosoft International, 3786 Corina Way, Palo Alto, CA 94303-4504. Preferred techniques for designing PCR primers are also disclosed in Dieffenbach and Dyksler, *PCR primer: a laboratory manual*, CSHL Press: Cold Spring Harbor, NY, 1995.--

In the Claims:

Claims 1, 3, 4 and 7 have been cancelled.

The following new claims have been added:

--31. An isolated polynucleotide comprising SEQ ID NO: 2076.

32. An isolated polynucleotide comprising a sequence selected from the group consisting of:

(a) complements of SEQ ID NO: 2076;

(b) reverse complements of SEQ ID NO: 2076; and

(c) reverse sequences of SEQ ID NO: 2076.

33. An isolated polynucleotide comprising a sequence selected from the group consisting of:

(a) sequences that are degeneratively equivalent to SEQ ID NO: 2076;

(b) sequences having at least 75% identity to SEQ ID NO: 2076;

(c) sequences having at least 90% identity to SEQ ID NO: 2076; and

(d) sequences having at least 95% identify to SEQ ID NO: 1076,

wherein the polynucleotide encodes a Myb transcription factor.

34. An isolated polynucleotide comprising a sequence selected from the group consisting of:

(a) nucleotide sequences that are 200-mers of SEQ ID NO: 2076;

(b) nucleotide sequences that are 100-mers of SEQ ID NO: 2076;

(c) nucleotide sequences that are 40-mers of SEQ ID NO: 2076; and

(d) nucleotide sequences that are 20-mers of SEQ ID NO: 2076.--

Claims 2, 5, 6, 8 and 13 have been amended as follows:

2. (Amended) An oligonucleotide probe or primer comprising at least 10 contiguous residues complementary to 10 contiguous residues of [a nucleotide sequence recited in claim 1] SEQ ID NO: 2076.

5. (Amended) An isolated polynucleotide that encodes a polypeptide [according to any one of claims 3 and 4] comprising a sequence selected from the group consisting of SEQ ID NO: 2346 and 2347.

6. (Amended) A DNA construct comprising a polynucleotide according to any one of claims [1 and] 5 and 31-34.

8. (Amended) A DNA construct comprising, in the 5'-3' direction:

(a) a gene promoter sequence,

(b) an open reading frame [coding for at least a functional portion of a polypeptide of any one of claims 3 and 4] of an isolated polynucleotide of any one of claims 5 and 31-34; and

(c) a gene termination sequence.

13. (Amended) A DNA construct comprising, in the 5'-3' direction:

(a) a gene promoter sequence,

(b) an untranslated region of an isolated polynucleotide of any one of claims [1 and] 5 and 31-34; and

(c) a gene termination sequence.